This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (currently amended) A method of using a mutation scanning array, wherein said mutation scanning array comprises a plurality of elements, wherein the elements contain immobilized oligonucleotides 8 - 50 bases long, that collectively span at least 10 different genes from the 5' to 3' end, wherein the genes can be either coding regions or the genomic genes, to identify mutations in a target DNA sequence which comprises:

(a) hybridizing the target DNA with a control DNA sequence to create a duplex, wherein the control DNA sequence is the wild-type DNA corresponding to the target DNA sequence, and wherein said target DNA comprises a pool of nucleotide segments that collectively span at least 10 different genes,

(b) tagging any mismatch in said duplex with a detectable moiety,

(c) cleaving the duplex into segments of 50 - 300 bases,

(d) removing the segments tagged with the detectable moiety,

(e) contacting the segments tagged with the detectable moiety with the mutation scanning array, and

(f) identifying in which gene and gene segment the selected mismatch belongs to.

2. (previously amended) The method of claim 1, wherein the segments tagged with the detectable moiety are amplified before being used on the mutation scanning array.

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